Gai, Lee
#8

1632

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/316,048

DATE: 04/19/2000
TIME: 10:13:02

Input Set: I316048.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

<110> APPLICANT: MOULAND, Andrew J.
COHEN, Eric A.
WICKHAM, Louise
LUO, Ming
DUCHAINE, Thomas
<120> TITLE OF INVENTION: MAMMALIAN STAUFEN AND USE THEREOF
<130> FILE REFERENCE: 10875-77
<140> CURRENT APPLICATION NUMBER: US/09/316,048
<141> CURRENT FILING DATE: 1999-05-21
<150> EARLIER APPLICATION NUMBER: CA 2,238,656
<151> EARLIER FILING DATE: 1998-05-22
<160> NUMBER OF SEQ ID NOS: 27
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO 1
<211> LENGTH: 3142
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3)..(1775)
<400> SEQUENCE: 1

ac ttc ctg ccg ggc tgc ggg cgc ctg agc gct ctt cag cgt ttg cgc 47
Phe Leu Pro Gly Cys Gly Arg Leu Ser Ala Leu Gln Arg Leu Arg
1 5 10 15

ggc ggc tgc gcc tct ctc tcg gct ccc gct tcc ttt gac cgc ctc ccc 95
Gly Gly Cys Al[illegible] Ala Pro Ala Ser Phe Asp Arg Leu Pro
30

ccc ccg gcc cc[illegible] c cgc ctc ttc 143
Pro Pro Ala A[illegible] u Arg Leu Phe
45

cct ccc ttc [illegible] ct tcc ttc ccc 191
Pro Pro Phe [illegible] er Ser Phe Pro
50 60

tcc tcg ccg [illegible] acg agc tcg gag 239
Ser Ser Pro [illegible] Thr Ser Ser Glu
65

cag cag cca [illegible] aat gca ctg tgc 287
Gln Gln Pro Glu Ser Ile [illegible] Asn Ala Leu Cys
80 85 95

atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct 335
Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser
100 105 110

cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc 383
Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro

Potential interference
09/286,959
although I made a
102(b) w/ Des Groseilliers et al
as evidenced by Wickham et al
and a 103 on the protein

```
45                  115                 120                 125
46      ccg agg tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa gtg   431
47      Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val
48              130                 135                 140
49      gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca aga   479
50      Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg
51          145                 150                 155
52      cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag   527
53      Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln
54      160                 165                 170                 175
55      aat gag ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa   575
56      Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu
57                      180                 185                 190
58      gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca   623
59      Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala
60                  195                 200                 205
61      ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc   671
62      Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly
63              210                 215                 220
64      cca ccc cac atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag ttt   719
65      Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe
66          225                 230                 235
67      gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc   767
68      Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala
69      240                 245                 250                 255
70      gcc ata gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca   815
71      Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala
72                      260                 265                 270
73      gtt gaa cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc   863
74      Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val
75                  275                 280                 285
76      aag cca cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc   911
77      Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser
78              290                 295                 300
79      cga ctg gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac   959
80      Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr
81          305                 310                 315
82      acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg   1007
83      Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met
84      320                 325                 330                 335
85      cag gtg aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag   1055
86      Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys
87                      340                 345                 350
88      aag gtg gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt   1103
89      Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly
90                  355                 360                 365
91      ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag   1151
92      Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu
93              370                 375                 380
94      gag aag aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc ttt   1199
```

```
Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe
    385                 390                 395
ttt gaa cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag gat   1247
Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp
400                 405                 410                 415
gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga att   1295
Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile
                420                 425                 430
ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga   1343
Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly
            435                 440                 445
cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc   1391
His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala
        450                 455                 460
acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg   1439
Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser
    465                 470                 475
ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac gta   1487
Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val
480                 485                 490                 495
ccc cat gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt tcc   1535
Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser
                500                 505                 510
aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac aac   1583
Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn
            515                 520                 525
aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct ctg   1631
Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu
        530                 535                 540
atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg gct   1679
Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala
    545                 550                 555
gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt aca   1727
Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr
560                 565                 570                 575
gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc   1775
Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys
                580                 585                 590
tgaacctttt ctggccatga accattataa aatcccaaca tatatactga aaatactgaa 1835
actgctttga aaatttggaa tttctgatac ctccagtggg ccgagagaca cggtgggtaa 1895
aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg 1955
gactgtgctg gggtttgttg tgatggccac tcggtgacct ggcggtccct acgcaatagc 2015
agctgcctgt ggggaagaag ggctgcccag ccagctggtt ctcccgggac accagcagat 2075
ccacaccctg ggcacctccg tgtttggtct ttttttccc ctgtgtgaaa gaagaaacgg 2135
cacgacccct tctcaagctg gctcactcag acacattggg acaaaccctg gacagccatg 2195
ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat caaatgcttc 2255
ctactcagcg tgacccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc 2315
acaccatcac cactgctttc tcttccaaca gtgatctgta ttcttagttt cattattttc 2375
ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat tgtatctagt 2435
taaatagcac agtttggaaa cttgtctgag actgacttta tcaataatct aaccgacaaa 2495
```

gatcatatcc atgtgtatgt ggttagacat ttttatttca ttgactaacc caggacagtt 2555
tcagtgatgc aaattgtgtg ccctctggtt cagctgaaac agtcctggac tttcaaaaac 2615
cttgaataag tctcccacag ttgtataaat tggacaattt aggaatttta aactttagat 2675
gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca ggacttaaat 2735
gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc 2795
ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct 2855
gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag 2915
aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtacacaga 2975
agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt 3035
aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa 3095
acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa 3142

<210> SEQ ID NO 2
<211> LENGTH: 591
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

Phe Leu Pro Gly Cys Gly Arg Leu Ser Ala Leu Gln Arg Leu Arg Gly
1 5 10 15
Gly Cys Ala Ser Leu Ser Ala Pro Ala Ser Phe Asp Arg Leu Pro Pro
20 25 30
Pro Ala Arg Arg Arg Pro Pro Pro Pro Arg Pro Leu Arg Leu Phe Pro
35 40 45
Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro Ser
50 55 60
Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu Gln
65 70 75 80
Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met
85 90 95
Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg
100 105 110
Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro
115 120 125
Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu
130 135 140
Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln
145 150 155 160
Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn
165 170 175
Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu
180 185 190
Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu
195 200 205
Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro
210 215 220
Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val
225 230 235 240
Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala
245 250 255
Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val
260 265 270

```
195         Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val Lys
196                 275                 280                 285
197         Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg
198             290                 295                 300
199         Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr
200         305                 310                 315                 320
201         Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln
202                         325                 330                 335
203         Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys
204                     340                 345                 350
205         Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe
206                 355                 360                 365
207         Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu
208             370                 375                 380
209         Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe
210         385                 390                 395                 400
211         Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu
212                         405                 410                 415
213         Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile Leu
214                     420                 425                 430
215         Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His
216                 435                 440                 445
217         His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr
218             450                 455                 460
219         Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro
220         465                 470                 475                 480
221         Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val Pro
222                         485                 490                 495
223         His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser Arg
224                     500                 505                 510
225         Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn Lys
226                 515                 520                 525
227         Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Ile
228             530                 535                 540
229         Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala
230         545                 550                 555                 560
231         Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu
232                         565                 570                 575
233         Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys
234                     580                 585                 590
235   <210> SEQ ID NO 3
236   <211> LENGTH: 3217
237   <212> TYPE: DNA
238   <213> ORGANISM: Homo sapiens
239   <220> FEATURE:
240   <221> NAME/KEY: CDS
241   <222> LOCATION: (363)..(1850)
242   <400> SEQUENCE: 3
243         acttcctgcc gggctgcggg cgcctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt 60
244         ctctctcggc tcccgcttcc tttgaccgcc tccccccccc ggcccggcgg cgcccgcctc 120
```

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/316,048**

DATE: 04/19/2000
TIME: 10:13:02

Input Set: **I316048.RAW**

Line	?	Error/Warning	Original Text
344	W	Invalid/Missing Amino Acid Numbering	
986	W	Invalid/Missing Amino Acid Numbering	